Please replace the paragraph at page 4, line 23, to page 5, line 1, as follows:

--The second aspect of the invention is the enzyme in the first aspect, having the amino acid sequence of SEQ ID NO. 7 in the sequence listing.--

Please replace the paragraph at page 5, lines 2-4, as follows:

--The third aspect of the invention is the gene encoding the enzyme in the first aspect, having the DNA sequence of SEQ ID NO. 8 in the sequence listing.--

Please replace the paragraph at page 16, lines 8-19, as follows:

--After the purified DyP was denatured by ordinary methods, partial hydrolysis thereof using trypsin was performed. Partially digested peptides thus formed were fractionated by HPLC. Consequently, five fragments were recovered. The amino acid sequence of each of the fragments was determined by the Edman method with a protein sequencer. Among the amino acid sequences of the resulting five fragments, the first sequence was Trp Lys. The amino acid sequences of the second and thereafter are shown in the sequence listing, where the second is shown in SEQ ID NO. 1; the third is shown in SEQ ID NO. 2; the fourth is shown in SEQ ID NO. 3 and the fifth is shown in SEQ ID NO. 4.--

Please replace the paragraph at page 16, lines 20-22, as follows:

--Among these amino acid sequences, a partial sequence (SEQ ID NO. 5) of SEQ ID NO. 3 and a partial sequence (SEQ ID NO. 6) of SEQ ID NO. 4 were selected as PCR primers.--

Please replace the paragraph at page 17, lines 11-15, as follows:

--The recombinant plasmid was amplified, by using E. coli JM 109 strain. From the resulting plasmid was cutout the coding gene. By a second PCR, the resulting DNA was sequenced (see the positions 1012 to 1181 of SEQ ID NO. 8 in the sequence listing).--

Please replace the paragraph at page 19, lines 1-8, as follows:

--This indicates that pB92 carries the DyP gene. The amino acid sequence of DyP and the nucleotide sequence of the DyP gene, carried in pB92, are shown as SEQ ID NOS. 7 and 8, respectively. In other words, DyP having the amino acid sequence described as SEQ ID NO. 7 in the sequence listing is the enzyme described in the second aspect of the invention, while the gene having the nucleotide sequence described as SEQ ID NO. 8 in the sequence listing is the gene in the third aspect of the invention.--

Please replace the paragraph at page 31, line 22, to page 32, line 8, as follows:

--Homology screening of the DyP gene (SEQ ID NO. 9) was carried out, by using three types of databases (Genebank, EMBL, DDBJ). Consequently, the peroxidase derived from U77073 (Polyporaceae sp.) registered at the Genebank, was screened, which was a gene homologous with DyP. Then, the homology between the two was examined. When regions with high homology were examined, the region at position 407 to position 438 was at the highest homology of 88 %, while the region at position 62 to position 85 was 83 % homologous. For the whole sequence of the gene, only 56 % homology was observed. Additionally, peroxidases with high homology, except for the peroxidase derived from Polyporaceae sp., were never found.--

Please replace the paragraph at page 32, line 18, to page 33, line 8, as follows:

--The classification by Welinder et al. is based on the comparison of highly common sequences in the primary sequence of each peroxidase. In more detail, the classification is practiced by comparing the primary sequences around the His residue proximal to the heme iron and the His and Arg residues distal to the heme iron. Using the sequence comparison table prepared by Welinder et al., the DyP sequence was compared (Fig. 4).